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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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		Post-processing:	Minimum DB seq Maximum DB seq	Searched: Total number of	Scoring table:	Title: Perfect score: Sequence:	ı	
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	•	% summaries		residues	0	:	model 158 ; Search time 6737 Sec (without alignments) 14847.312 Million ce	2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a

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ALIGNMENTS

AUTHORS TITLE	REFERENCE	SOURCE ORGANISM	ACCESSION VERSION KEYWORDS	LOCUS	RESULT 1 AX468679
Gao, W.Q., Polakis, P., Shou, J., Smith, V., Soriano, R., Williams, P.M., Wu, T.D. and Zhang, Z. Compositions and methods for the diagnosis and treatment of tumor	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1	human, HOmo sapiens	AX468679 AX468679.1 GI:21901457	AX468679 3437 bp DNA linear PAT 16-JUL-2002 Sequence 3 from Patent W00216581.	

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2820 2820	61 CTGAGTGACATAGACGAGAT	, N 1
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2700 2700	41 TCAGCCGGCTCCTTGCCCCTGGTCAGCGTCTGCCTGTTCACCCTCTGACCGCGGCCGAG	
2640 2640	81 CTGCCCAGCAGGACGACGACGACGACGACGACGAGGACGAAGAGGGCGAGGAG	
2580 2580	SZI GACCTGTCCTTC	
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2460 2460	OL AAGTCCTCCCGCCATCTGGCT	
2400 2400	341 CACCAGGGGGCGCTGTGGGACT	
2340 2340	281 TGCTTCCTGCACGTGCTGC	
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                                                                                                                                                                                                                                                                                                                            Submitted (31-Jan-2000) Osamu Ohara, Kazusa DNA Research Institute, Laboratory of DNA Technology; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:cdmainfo@kazusa.or.jp, URL:http://www.kazusa.or.jp/huge/, Tel:+81-438-52-3913,
                                                                                                                                                                                                                                                                                                                                                                                                                 Ohara, O., Nagase, T. and Kikuno, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nagase,T., Kikuno,R., Ishikawa,K.I., Hirosawa,M. and Ohara,O. Prediction of the coding sequences of unidentified human genes. XVI. The complete sequences of 150 new cDNA clones from brain which code for large proteins in vitro DNA Res. 7 (1), 65-73 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens brain cDNA to mRNA, clone_lib:pBluescriptII SK plus clone:hg02441b.
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Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.
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/product-"HAA1440 protein"
/protein_id="BAA92678.1"
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/translation="AAASTKQTITESSSLLLSQLTSLDPQGPPRRPPPHILDQVKSLN
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ORIGIN BASE COUNT 731 a FEVVOTALIRILFEYALLCQEHAAVILHRAFIVGMYGQMDPSAQISEALRILHMEAVM

δõ 밁 δÃ 밁 Qy 밁 8 밁 QΨ 밁 ΩV 밁 Ş 及 Qγ 밁 δĀ. 맑 Qγ Ş 밁 밁 Ş Query Match Best Local Similarity Matches 3433; 1600 1540 1480 1420 GCCCACCTGGTGGAGGTCCAGCATGAGCGCGGGGGGCCTCCGGAGGCCAGACTTTCCACTCC 1479 1300 1180 661 CGGTGGCAGAGCTCCAGTCCCGGCCCGTGGCCCTCGCCCTGCAGCAGGCCCTGGGCCAG 720 1120 CAGGCGCTGCTGGACATCTGGTTTCCGGAGGAGAAGCCACTGCCCACCGCCTTCCTGGTG 1179 601 1360 1000 CAGGACCAGGTCTTCCTACGCTGGAGCAGCGGGGAGACAGCCACCATGCACATCCTCGTG 1059 541 481 421 GCCCACCTGGTGGAGGTCCAGCATGAGCGCGGGGGGCGCCTCCGGAGGCCAGACTTTCCACTCC 480 361 CAGGCAGTGGCCCACGACCCCCAGACTCTGGAGCAGAACATCATGGACAAGAATTACATG 420 301 TTCGTGCAGTCGTTTGGCATCCCCGTGTCCAGCATGAGCAAACTCCTCCAGTTCCTGGAC 360 241 121 CAGGCGCTGCTGGACATCTGGTTTCCGGAGGAGAAGCCACTGCCCACCGGCTTCCTGGTG 180 181 1 CAGGACCAGGTCTTCCTACGCTGGAGCAGCGGGGAGACAGCCACCATGCACCATGCACCATGCTCGTG 60 AGCCCAGAGCAGCCATAGGCCAGGGCCGGATTCGGGTGGGGACCCAGCTCCGGGTGCTG 600 TTGCTCACAGCCTCCCTGCCGCCCGCCGAGACAGCACAGAGGCACCCAAACCAAAGAGC 1539 GGCCCTGAGGACGACCTGGCTGGCATGTTCCTCCAGATTTTCCCGGCTCAGCCCGGACCCT 1659 GGCCCTGAGGACGACCTGGCTGGCATGTTCCTCCAGATTTTCCCGCTCAGCCCGGACCCT 660 TTGCTCACAGCCTCCCTGCCGCCCCGCGAGACAGAGCACAGAGGCACCCAAACCAAAGAGC 540 TICGIGCAGICGITIGGCATCCCCGIGTCCAGCAIGAGCAAACICCICCAGITCCIGGAC 1359 GAGGTGCTCCGCCTGGTGGACGCCGCCCTGCAGGACCTGGAGCCGCCAGCAGCTGCTGCTG 300 GACACATOGGAGGAGGCGCTGCTGCTTCCTGACTGGCTGAAGCTGCGCATGATCCGTTCT 1239 GACACATCGGAGGAGGGCTGCTGCTTCCTGACTGGCTGAAGCTGCGCATGATCCGTTCT 240 Conservative 99.8%; Score 3431.8; 99.9%; Pred. No. 0; 0; Mismatches DB 9; 2; Indels Length 4434; 0; Gaps 1299 0

41 GTCCARGGCTCGGAGGTGATGATGATGATGATGATGATGATGATGATGATG	17	
AIL	Db 268	
20 CAGAGGTTCGACCCCTCTGCCTCTCGGA	. 26	
21 CAGAGGTTCGACCCTCTCGCCTCTCTGGACTTCCTCTGGGCCTGCATCCATGTTCCTCGC 168	Qy 16:	
60 CAGTCCAGCTGGCCCACACTGCACCAGTGCATCCGAGTCCTGCTGGGCAAGAGCCGGGAA 261	Db 25	
61 CAGTCCAGCTGGCCCACACTGCACCAGTGCATCCGAGTCCTGCTGGGGCAAGAGTCCGGG	Qy . 15	
UL GUCARAGGTCAGGCCAGGTGCCCTGCTTCCGTTCCCTACCTCCTGACCCTCTTCAGGCAT 156 00 GGCARAGGTCAGGCCAGGTGCCCTCGTTCCGTTCCTGACCCTCTGACCCTTCTTCACGAT 255 00 GGCARAGGTCAGGCCCCAGGTGCCCTTCGTTCCGTTCCTTGACCCTTACCTCTTCACCATTCACTCACTTCACCATTCACCATTCACCATTCACTTCACCATTCACTCACTTCACTTCACTTCACTCACTTCACTTCACTTCACTTCACTCACTTCACACTTCACTTCACTTCACTTCAC	Db 25	
40 CCCAGGTGGTCAGCAGCTGCCCCGACCTGCAGCTCAGGCTGCTCTTCTCCCGGAGGA	24	
CCGAGGTGGTCAGCAGCTGCCCCGACCTGCAGCTCAGGCTGCTCTTCTCCCGGAGGAAG 150		
	23	
381 GAGGCCGTGCGCTGGGGCCCTCGTCATCATCATCATCATCATCATCATCATCATCATCATCAT	13	
	N	
321 CTGCTGCAGGAGGAGGACCCCCTGGCTGGGGTGAGAAGCCCCCCTGCCCTTGCCCTGCCCTGCCCCTGCCCTGCCCTGGGTGAGAGCAGCCCCCTG	Ωу 13	
260 ACTGCGGATGCTGCCCCGTTTCCAGCCTGTAAGCCCGTTGTGGTGGTGAGCTCCCTG 132	N H	
261 ACTOCOCATIONICATES TO AN ACTOCOCATION OF THE STATE OF		
1201 GGCTGATCGAGGTGAGGTGACCCCCCCCCCCCCGAGGGAGCTGCTGACTGCATTCTCTCTC	3 t	
140 ACCCTGAGGTCTGGGGAGCAGTGCAGCGTGGAGCC	א י	
41 ACCCTGAGGTCTGGGGAGCAGTGCAGCGAGCGTGGAGCCGACCTGATCAGCAAAGTCCTCC	Qy 11	
080 GCCCTGGCCTTCCGTCAGGACCTGGAGGTGGTCAGCTCCACCGTCCGT	N	
081 GCCCTGGCCTTCCGTCAGGACCTGGAGGTGGTCAGCTCCACCGTCCGT	Qy 1(
02	N	
021 CAGGCCTCAGCCGGGCCCAGGCTCAGTGAGTGAGTGAGCCCCCCCTCCTTCCT	Qy 10	
96	H	
CAT ASTERMALTSTRUCKSTONES CONTRACTOR CONTRAC		
10 CARCAGGACACCGGCTTCTCCCTCCTTCTCTCAAGGTGCTCCAGATGCTGCAGTTGCAGTAGCTTCCTCCAGTAGCTTCTTCTCAAGGTGCTTCTTCTTCTTCAGTAGTTCTTCTTCTTCAGTAGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTC	Db 1:	
840 CGTAGCCACTTCCTGGCCTGCCCGCTGCTGCGCCAGCTCTGCCC	, _–	
841 CGTAGCCACTTCCTGGCCTGCCCGCTGCTGCGCCAGCTCTGCCAGTACCAGCGCTGTGT	,	
ATGCAC 18		
AGGCCCTCGCCACCCTGCTCAGCTCCCCACACGCGGTGCCCTGGTGATGTCCATGCAC	Qy	
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	D)	

Db 2740 GPCCAGGGCCCGAGCTCAGCCTGAGCCTGAGCCCGAGGCAGGCAGGAGG
2740 GTCCAGGGCCGGAGCTCATCCAGCCTGGAGCTGAATCCTGGCCGAGGCGGAGACCGAGCCGAGACCGGAGCCGAGCCGAGCCGAGCCGAGCCGAGACCGAGCCGAAACCACC
ITGATTCCTGGCCGAAGCCGAGACC

DЬ	Qy	Дb	Qy	Db	δĀ	₽	ΔÃ	Дδ	Qy	DЪ	Qγ	Дb	δÃ	В	ΔĀ	DЪ	V	DЬ	Qy
4420	3421	4360	3361	4300	3301	4240	3241	4180	3181	4120	3121	4060	3061	4000	3001	3940	2941	3880	2881
ACGACCTGAACTGTC 4434	ACGACCTGAACTGTC 3435		ACAGCCCTGCCGGAGCGGCGGATCCCCCCGGGCATGGCCTGGGCTGGTTTTGAATGAA	CTCCGGGCCGGCCGCTGGCATCAGGGCCCTCCAGCAAGCCCTCATTCACCTTCTGGGCC 4359	CTCCGGGCCGGCCGTGGCATCAGGGGCCGTCCAGCAAGCCCTCATTCACCTTCTGGGCC 3360	GAGGGCGCCGAGCCCTGAGGCCAGGCAGGCCCAGGAGCAATACTCCGAGCCCTGGGGTGG 4299	GAGGGCGCCGAGCCCTGAGGCCAGGCAGGCAGGAGCAATACTCCGAGCCCTGGGGTGG 3300		CCGGGGATCCTCGAGGAAAGCCCAGGAAGCGTGGGCGTTGCTGGTCTGTCCGAGGAGGT 3240		GAGGCCGTGATGTGAGCCTGTGGCAGCCGACCCCCCTCCAAGCCCCGGCCCGTCCCGTCC 3180	ATGTACGGCCAGATGGACCCCAGCGCGCAGATCTCCGAGGCCCTGAGGATCCTGCATATG 4119	ATGTACGGCCAGATGGACCCCAGCGCGCAGATCTCCGAGGCCCTGAGGATCCTGCATATG 3120	TACGCTCTCCTGTGCCAAGAGCACGCGGCTGTGCTGCTGCTGCACCGGGCCTTCCTGGTGGGC 4059	TACGCTCTCCTGTGCCAAGAGCACGCGGCTGTGCTGCTCCACCGGGCCTTCCTGGTGGGC 3060			GCCTGCGCTCCATGCAGAACAGCCCCAGCATTGCAGCCGCTTTCCTGCCCACGTTCATG	

REFERENCE AUTHORS TITLE SOURCE ORGANISM RESULT 3
BC004286
LOCUS
DEFINITION
ACCESSION VERSION KEYWORDS JOURNAL Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 4179) 4179 bp mRNA linear PRI 12-JUL-2001 Homo sapiens, clone IMAGE:3618123, mRNA, partial cds. BC004286.1 GI:13279124 Homo sapiens.

REMARK

COMMENT

Strausberg,R.

Direct Submission

Submitted (01-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

(NIH-MGC Project URL: http://mgc.nci.nih.gov
 Contact: MGC help desk
 Email: cgapbs-rémail.nih.gov
 Tissue Proquement: ATCC/DCTD/DTP
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
 DNA Sequencing by: Genome Sequence Centre,
 Cancer Agency, Vancouver, BC, Canada
 info@bogsc.bc.ca
 Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
 Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
 Letticla Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
 Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven

Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Sacedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 3280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                           301 TTCGTGCAGTCGTTTGGCATCCCCGTGTCCAGCATGAGCAAACTCCTCCAGTTCCTGGAC 360
                                                                                                                                                                                                                               1047
                                                                                                                                                     1107 GAGGTGCTCCGCCTGGTGGACGCCGCCCTGCAGGACCTGGAGCCAGCAGCTGCTGCTG 1166
421 GCCCACCTGGTGGAGGTCCAGCATGAGCGCGGCGCCTCCGGAGGCCAGACTTTCCACTCC 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGS
                                                                                                                                                                                                                                                                           241 GAGGTGCTCCGCCTGGTGGACGCCGTGCAGGAGCTGGAGCCGCAGCAGCAGCTGCTG 300
                                                                                                                                                                                                                                 181 GACACATCGGAGGAGGCGCTGCTGCCTGCCTGACTGGCTGAAGCTGGCGCATGATCCGTTCT 240
                                                                                                                                                                                                                                                                                                                                                                                                    927 GTCCATGCCATGGTGATCCTGCTGACGCTGGGCCCGCCTCGAGCCGACGACAGCGAGGTTC 986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                                                                                                                                                                                                                                        61 GTCCATGCCATGGTGATCCTGCTGACGCTGGGCCCGCCTCGAGCCGACGACGACGGGTTC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                 GACACATCGGAGGAGGCGCTGCTGCTTCCTGACTGGCTGAAGCTGCGCATGATCCGTTCT 1106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILML at: http://lmage.llnl.gov Series: IRAL Plate: 13 Row: j Column: 11 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        analysis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FGIPVSSMSKLLQFIDQAVAHDPQTLEONIIMKNYKAHILVEQHERALEFWALLEFWA
TASLIPPREDSTEAFKPKSSPEQPIGQGRIRVGTQLRVLGPEDDLAGMELQIFPLSIDP
RWQSSSRPPVALALQQALGQELAKVVQGSPEVPGITVRVLQALATILISSPHGGALVMS
HRSSSFLACPLLAGLCQYQRCVPQDTGFSSLFLKVLLQMLQMLDSPGGGPLRAQLR
MLASQASAGRRLSDVRGGLLRLAERLAFRQDLEVVSSTVRFQPVSPLWW"
1 1412 c 1337 g 718 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="Vector: pOTB7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tissue_type="Skin, melanotic melanoma."
/clone_lib="NIH_MGC_20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'clone="IMAGE:3618123"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 3114.2;
Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 9;
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10 18 10 10 11 11 11 11 11 12 12 12 13 13 13 13 13 13 13 13 13 13 13 13 13	18 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9
021 021 081 01 01 01 01 01 01 01 01 01 0	1287 481 1347 541 1407 601 1467 661 1527 721 1587 7781 1587 7781 1587 779 1791
CAGGCCTCAGCCGGGCGCAGGCTCAGTGATGTGCGAGGGGGGCTCCTGCCCTGCCCTGCCCTCAGCCGGGCGCCTCAGCCGGGCGCCAGGCTCAGTGATGCTTGCCCCTGCCCTGCCCTGGCCTTGCCCTGGGCCTCAGCCGGGCGCCTCAGCCAGGCTCCTGCAGCTGCTCCAGCCTTCCGTCAGGACCTGGAAGGTGCTGCAACGTCCACCTTCCGTCAGCAAAGTCCTCCTCCTCCTCCTGCAGCTTCCGGAAGCTCCTGCAACGTCCTCCTCCTCCTCCTGCAGCTTCCGGAAGCTCCTGCAAAGTCCTCCTCTCCTGCAGCTTGCGAGCTTGCAGCTTGCAGCTTGCTGCTCCTCTCTCT	
GC 1886 AG 1946 AG 1946 AG 1946 AG 1200 199	

2640 3352	2381 CTGCCCARCAGGGACGACAGGACCGACCGAGGCCTGGACGAAGAGGGCGAGGAGGAGGAGAAGAGGGCGAGGAGAAGA	물 등
2580 3292	3233 GACCTGTCCTTCGACAACAGGTGACCTGGTGAAATCCCTCCTTGCAGGGCTCAGC	, B 7
2520 3232	2*01 ATTACCTACAATIGCCCCAGCAGCAGCATCTCCTTCCTGCAGAAGCACGCCGACCCGCTCCAC	Q B 4
2460 3172	2401 AMSTRUTECCGCCATCTGGCTGCCTTCATCAACAAGTTT	
2400 3112	31 LACTORES COLORS OF A CALCARD COLORS OF A CA	א ש פ
2340 3052	2201 THE THE CONTROL OF THE ACCORDANCE OF THE ACCORDACIONE OF THE ACCORDANCE OF THE) U K
2280 2992	221 CTCCUGCACGGCCGCACCCACCTCAACTTCCAGGAC	א ט ג
2220 2932	2151 CGGAAGCTGGCGGTGGCGCACCCGCTGCT	
2160 2872	2101 GUGGACACCAGUGACTCCCGGGCC) H r
2100 2812	041 GCTGCCAGCAGCAGCGTCTGCAAGCTGGACGGJ	
2040 2752	1981 TACCTACAGCGGCCGGAG	
1980 2692	1921 ATCCAC	
1920 2632	1861 AGCTGCT 11 2573 AGCTGCT	
1860 2572	1801 AGCCAGGA 2513 AGCCAGGA	
1800	741 GTCC	
1740 2452	168 239	
: 1680 : 2392	1621 CAGAGGTTC	
1620	156 227	
2272	2213 GGCAAAGGTO	

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ДЬ	Qy	당 성	문	Qγ	В	Qy	Db .	¥0	망	Qγ	뭥	Ϋ́	B	Qy	DЬ	Qγ	В	δÃ	В	QΨ	В	Qy	Db	VQ	뮹	Qy
4133	3421	4073	013	3301	3953	3241			3833	3121	3773	3061	3713	3001	3653	2941	3593	2881	3533	2821	3473	2761	3413	2701	3353	2641
ACGACTGAACTGTCAA 4149	3437	ACACUCTECCECEGACCEGCGATCCCCCCGGCCATGGCCTGGGCTGGTTTTGAATGAA		CTCCGGGCCGGCCGCTGGCATCAGGGGGCCGTCCAGCAAGCCCTCATTCACCTTCTGGGCC 3360	GAGGGCGCGAGCCCTGAGGCCAGGCAGGCCCAGGAGCATACTCCGAGCCCTGGGGTGG 4012	330					ATGTACGGCCAGATGGACCCCAGCGCGCAGATCTCCGAGGCCCTGAGGATCCTGCATATG 3832		TACGCTCTCCTGTGCCAAGAGCACGCGGCTGTGCTGCTCCACGGGCCTTCCTGGTGGGC 3772		TACTECCTGGGCAGCCAGGACTTTGAGGTGGTGCTGCAGACGGCCCTCCGGAACCTGCCTG	TACTGCCTGGGCAGCCAGGACTTTGAGGTGGTGCAGACGGCCCTCCGGAACCTGCCTG	GCCCTGCGCTCCATGCAGAACAGCCCCAGCATTGCAGCCGCTTTCCTGCCCACGTTCATG 3652	GCCCTGCGCTCCATGCAGAACAGCCCCAGCATTGCAGCCGCTTTCCTGCCCACGTTCATG 2940	AACCTGCAGCGGCTGATGAGCTCGGCCCAGGAGTGTTGCCGCAACCTCGCCTTCAGCCTG 3592	AACCTGCAGCGGCTGATGAGCTCGGCCCGAGGAGTGTTGCCCCCAACCTCGCCTTCAGCCTG 2880	CTGAGTGACATAGACGAGATGTCCCGGGGGGAGACCCGAGATCCTGAGCTTCTCCGACC 3532	CTGAGTGACATAGACGAGATGTCCCGGGGGAGACCCGAGATCCTGAGCTTCTTCTCGACC 2820	ATGGCCCCCTACATGAAACGGCTTTCCCGGGGCCAAACGGTGGAGGATCTGCTGGAGGTT 3472	ATGGCCCCCTACATGAAACGGCTTTCCCCGGGGCCAAACGGTGGAGGATCTGCTGGAGGTT 2760	TCAGCCGGCTCCTTGCCCCTGGTCAGCGTCTCCCTGTTCACCCCTCTGACCGCGCCGAG 3412	

REFERENCE AUTHORS TITLE JOURNAL

RESULT 4
BC013367
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Homo sapiens.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2769)
Strausberg,R.
Direct Submission
Submitted (31-AUG-2001) National Institutes of Health, Mammalian BC013367 2769 bp mRNA linear PRI 04-SEP-2001 HOMO Sapiens, clone IMAGE:3677373, mRNA, partial cds. BC013367 BC013367.1 GI:15426515

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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 2732;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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189 GTACCAGCGCTGTGTGCCACAGGACACCGGCTTCTCCTCGCTCTTCCTGAAGGTGCTCCT 248
                          885 GTACCAGCGCTGTGTGCCACAGGACACCGGCTTCTCCTCGCTCTTCCTTGAAGGTGCTCCT 944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
                                                                                                                                     129
                                                                                                                                                                                          825
                                                                                                                                                                                                                                                                        765 CACGGTGCGTGTCCTGCAGGCCCTCGCCACCCTGCTCAGCTCCCCACACGGGGGGTGCCCT 824
                                                                                                                                                                                                                                                                                                                                                                                       705 GCAGGCCCTGGGCCAGGAGCTGGCCCGCGTCGTCCAGGGCAGCCCCGAGGTGCCGGGCAT 764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                              69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 79.2%;
Local Similarity 99.9%;
                                                                                                                                                                                                                                                                                                                               GGTGATGTCCATGCACCGTAGCCACTTCCTGGCCTGCCCGCCTGCTGCGCCAGCTCTGCCA
                                                                                                                                                               GGTGATGTCCATGCACCGTAGCCACTTCCTGGCCTGCCGCTGCTGCGCCAGCTCTGCCA 884
                                                                                                                                                                                                                    CACGGTGCGTGTCCTGCAGGCCCTCGCCACCCTGCTCAGCTCCCCACACGGCGGTGCCCT 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINI at: http://image.llnl.gov Series: IRAL Plate: 24 Row: m Column: 10 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Institute for Systems Biology http://www.systemsbiology.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                analysis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             confact: amadan@systemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        462 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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LRMLASQASAGRRLSDYRGGILRIAEALAFRODLEVVSSTYRAVIATILKSGRQCSYEP
DLISKYLQGLIEVRSPHLEELLTAFFSARTADAASPFPACKPVYVSSILLOEEEPLAG
GKCAJAGGSGLAVRIACAPSSGLIVPMLEMLDFEDVYSSCPDLOLRILFSRKGKQAQYP
GKFRYLLILFTHQSSWPTLHQCIRVLIKAEBEFRODGSASLDFIMACHHYPRIWGGRD
QRTPOKRREELVLRYQGPELISIVELILAEAFFRSQDGDTAACSLIQARLFILLSCCC
GDDESVRKTYTEHLSGCIQOWGDSVLGRRCKDLLLQLIVGREKPVPFEVLLHSEGAA
LLHGRTHINFQDEFQQNHLSCEHHYLGLEELLQPHVFRSEHQGALWDCLLSFTRLLLA
YKRSSRHLAAFINKFYQFIKKTITYAAFAAISFLQCHADFHDLSFONSDLVMLKSLL
YKRSSRHLAAFTNKFYDFIKKTITYAAFAAISFLQCHADFHDLSFONSDLVMLKSLL
YKRSSRHLAAFTNKFYDFIKKTITYAAFAAISFLACHADFHDLSFONSDLVMLKSLL
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EDLLEVLGDIDEMSRRPEILSFFSTNLQRLMSSAEECCKNLAFSLALRSWQNSPSIA
AAFLFTENYCLGSQDFEVYGTALKNLPEYALLCQEHAAVLLHRAFLYGMYGQMDPSAQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="Unknown (protein for IMAGE:3677373)"
/protein_id="AAH13367.1"
/db_xref="GI:15426516"
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/clone_lib="NIH_MGC_8"
/lab_host="DH10B-R"
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/db_xref="taxon:9606"
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                                                                                  GCACCTGTCAGGCTGCATCCAGCAGTGGGGAGACAGCGTGCTGGGCAGGCGCTGCCGAGA 1268
                                                                                                                                            GCTGCCCCTGCTGCTGCTGCTGCTGGGGGACGATGAGAGTGTCAGGAAGGTGACGGA 1208
                                                                                                                                                                       GCTGCCCCTGCTGCTCAGCTGCTGCTGTGGGGACGATGAGAGTGTCAGGAAGGTGACGGA 1904
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	3104 2408	2349 GGCCTTCCTGGTGGGCATGTACGGCCAGATGGACCCCAGCGCAGATCTCCGAGGCCCT	
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	2 22	CHGCCCACGTTCATGTACTGCCTGGGCAGCCAGGACTTTGAGCTGTTGCAGGCGGCCT CGGAACCTGCCTGAGTACGCTCTCTCTGTGTCTAAGAACACACGCCTTTTGAGTGCTAGGAGGCCCTT	0 -
	9	2925 CCTGCCCACGTTCATGTACTGCCTGGGCAGCAGCAGCACTTTGAGGTGGTGCAGACGGC	
	292 4 2228	Db 2169 CCTCGCCTTCAGCCTGGGCCCTGCGCTCCATGCAGAACAGCCCCAGCATTGCAGCCGCTTT Db 2169 CCTCGCCTTCAGCCTGGCCCTGCGCTCCATGCAGAACAGCCCCAGCATTGCAGCAGCGCTTT	
	2864 2168	2109 GAGCTTCTTCTC	
	2804 2108	2049 GARCETTOTTOTTOTTOTTOTTOTTOTTOTTOTTOTTOTTOTTO	
	2048	CTGACCGCGGCCGAGATGCCCCTACATGAAACGGCTTTCCCGGG	_
	74	2685 TCTGACCGCGGGCCGAGATGGCCCCCCTACATGAAACGGCTTTCCCCGGGGCCAAACGGTGG	
	2684 1988	Db 1929 GGCCAGGAGAGACCTCAGCCGCTCCTTGCCCCTGGTCAGCGTCTCCCTGTTCACCCC	
	92	1869 CCTTGCAGGGCTGCCCAGCAGGACGACAGGACCGACCGAGCCTGGACGAAG	
	60 0	CTTGCAGGGCTCAGCCTGCCCAGCAGGGACGACGACGACGACGACCGAC	
	2564 1868	80	
	80	1749 GTTCATCATAAGTACATTACCTACAATCCCCCAGCAGCCATCCCTTCC	
	50	CATTACCTACAATGCCCCAGCAGCCATCTCCTTCCTGCAGAAGC	
,	2444 1748	Db 1689 GCTGCTGAATTACAGGAAGTCCTCCCGCCATCTGGCTTCCTTC	
	68	1629 CGTGTTCCGCAGCGAGCACCAGGGGGCGCTGTGGGACTGCCTTCTGTCCTTCATC	
	ن ت	GTGTTCCGCAGCGAGCACCAGGGGGGGCGCTGTGGGACTGCCTTCTGTCCTTCATCCGC	
	2324 1628	0 0	
	2264 1568	220 GUCANGATGGGGGGGCTCCTGCAGGGCGGACCGACCTC	
	50	1449 TGCCAGCATGGCCTGCCGGAAGCT	
	220	TGGCCTGCTGGCAAGCTGGCGGTGGCGCACCCGCTGCTGCTGCTCAGGCACC	
	2144	QY 2085 CTTCATCACGCTCCTTGCGGACACCAGCGACTCCCGGGCGTTGGAGAACCGAGGGGGGGAGACCGAGGGGGGGG	
	1388	1329 ACTGCAC	

FEATURES

source

Location/Qualifiers

/Organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4869992"
/tissue_type="Skin, melanotic melanoma, high MDR."
/clone_lib="NIH_MGC_49"
/lab_host="DH10B-R"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINI at: http://Image.llnl.gov series: IRAL plate: 40 Row: k Column: 14
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                   Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                                                                                                  CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (07-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tissue Procurement: ATCC/DCTD/DTP
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2418)
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1579 CTGCACCAGTGCATCCGAGTCCTGCTGGGCAAGAGCCGGGAACAGAGGTTCGACCCCTCT 1638
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                                                                                                               Berlin-Charlottenburg, GERWANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available
                                                                                                                                                         Please contact the RZPD: Ressourcenzentrum,
                                                                                                                                                                         This clone (DKFZp586J0619) is available at the RZPD in Berlin
                                                                                                                                                                                        sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing consortium of the German Genome Project.
                                                                                                                                                                                                                            Martinsried, GERMANY Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s. Wiemann@dkfz_heidelberg.de;
                                                                                                                                                                                                                                                                                    Submitted (10-MAR-1999) MIPS, Am Klopferspitz 18a, D-82152
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Homo sapiens mRNA; cDNA DKFZp586J0619 (from clone DKFZp586J0619);
partial cds.
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/clone="DKFZp586J0619"
/tissue_type="uterus"
                                  /organism="Homo sapiens"
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/ CHANGE STERMEL. 19Y3W8 "

AGKFORD GGSLEAVRLOFESGLLVWLEMIDDEVYSSCDED, DLELLE SERRÖKGORO, VESFREYLLTILFTHOSSIPPLHOCI KYULGKSERGEDDESASLIDETWACHTWPLINGE GORO ROFFERVELTILTENGE GLOOMODS VLGRECHDELLOCKLOFELERVEYPFYLLILESG COGDDESVRKYTEHLSGCLOOMODS VLGRECHDLLLOCKLOFELERVEYPFYLLILESG AASSVCKLDOLI HREFTLLADYSDSRALENGALASMACKLAVARPLLIKHEND AALHGRITHLAPGEROONHLSCFLHVLGILLELLOPHYERSEHOGALMDCLLSFIRL LINYRKSSRHLAAFINKFVOFTHY AT TYNAPAALSFIQATHDFHLSFONSDLYMLKS

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DH10B; sites NotI + SalI/MluI"
,dev_stage="adult"
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/protein_id="CAB43278.1"
/db_xref="GI:4884140"
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	1699		Дb
	2 0	2851 GAGTGTTGCCGCAACCTCGCCTTCAGCCTGGCCTCTGACCTTCATCTTTATCTTCATCTTCATCTTCATCTTCATCTTCATCTTCATCTTTCATCA	δÕ
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	ν	280 TTCCTGCAGAAGCACGCCGACCCGCTCCACGACCTGTCCTTCGACAACAGTGACCAGTGACCTGGT 551 ATGCTGAAATCCCTCCTTGCAGGGCTCAGCCTGGCCAGCCA	מ מ
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	859	800 GTGCCTGAGGTCCTACTGCACAGCGAAGGGGCTGC	<u> </u>
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               CGGGCATGGCCTGGGCTGGTTTTGAATGAAACGACCTGAACTGTCAA 3437
TCCAGCAAGCCCTCATTCACCTTCTGGGCCACAGCCCTGCCGGGAGCGGCGGATCCCCC
                                         TCCAGCAAGCCTCATTCACCTTCTGGGCCACAGCCCTGCCGGGGGAGCGGGGGGATCCCCC 3390
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SOURCE RESULT 7 BC010333 LOCUS KEYWORDS VERSION DEFINITION

2730 bp mRNA linear H BC010333 GI:16307573 ROD 07-AUG-2002

REFERENCE AUTHORS TITLE JOURNAL

> Mus musculus house mouse.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 2730) Direct Submission

COMMENT REMARK

NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Tissue Procurement: Gilbert Smith, Ph.D. Submitted (05-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome Center code: BCM-HGSC Sequencing Center

Web site: http://www.hgsc.bcm.tmc.edu/cdna/Contact: amg@bcm.tmc.edu

Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M., Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M., Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 16 Row: n Column: 18
This clone was selected for full length sequencing because it

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Best Local
1167 CGTGGAGCCGGACCTGATCAGCAAAGTCCTCCAGGGGCTGATCGAGGTGAGGTCCCCCCA 1226
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TLALAHHSHELSOPLARQLIQQYQRAVPQDTGFSSLFLKVLAQILQWLDSPAYEDGFL
QAQLKLFATRYSARHRISDVRSGLLHLADALSFHGDLEVANSTRARVLATLASGERCP
VEPELISKVLAGLIEVRSPHLEELLTALLFRAYETSCPSPASGPAVVLATLASGERCP
LIGPSKQEVEGASTEAMRLGPASGLLVDWLETLDPEVVCSCPDLQWKLLFSRRGKCH
ISAQVLSFRPYLLALLTHQASWSTLHRCIKVLLGKEREQKLDPSASLDFLWACIHVPR
IWQGRDQRTPQKRREELYLHVQGPELISLVELILSEAFTRSQDGDSAARTLIQTRLDL
TSAQVLSFRPYLAALLTHQASTEHACITVLLGKEREQKLDPSASLDFLWACIHVPR
IWQGRDQRTPQKRREELYLHVQGPELISLVELILSEAFTRSQDGDSAARTLIQTRLDL
TOTAL TOT
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/protein_id="AAH10333.1"
/db_xref="GI:16307574"
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/db_xref="taxon;10090"
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Pred. No. 1.7e-236;
0; Mismatches 435;
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Ansorge,W., Wirkner,U., Mewes,H.W., Gassenhuber,J. and Wiemann,S
                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1141)
                                                                                        Homo sapiens
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                                                                                                                                                                          Homo sapiens mRNA; cDNA DKFZp434C0126 partial cds. AL137358
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CTCCCTGTTCACCCCTCTGACCGCGGCCGAGATGGCCCCCTACATGAAACGGCTTTCCCCG 420
                                                                            AGCCTGGACGAAGAGGGGAGGAGGAGCTCAGCCGGCTCCTTGCCCCTGGTCAGCGT
                                                                                                                                                     GTCCTTCATCCGCCTGCTGCTGAATTACAGGAAGTCCTCCCGCCATCTGGCTGCCTTCAT 2429
                                                                                                                   AGGCCTGGACGAAGAGGGCGAGGAGAGCTCAGCCGGCTCCTTGCCCCTGGTCAGCGT
                                                                                                                                                                                                                                      CTTCCTGCAGAAGCACGCCGACCGGCTCCACGACCTGTCCTTCGACAACAGTGACCTGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone (DKFZp434C0126) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 140: Berlin-Charlottenburg, GERWANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is availat http://www.mips.biochem.mpg.de/proj/cDNA/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission Submitted (15-JAN-2000) MIPS, Am Klopferspitz 18a, D-82152
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DEGGEESSAGSLETMSVSLIFTPLTAARMAPYMKRLSRGGTVSDLLEVLSUDIDEMSRR
RPEILSFFSTMLORLMSSABECCRNLAFCLALRSMQNSPSIAAAFLFFFMYCLGSQDF
EVVQTALRNLPEYALLCQEHAAVLHRAFPGGHVREDGFQRADLRGFEDFAYGGRDVS
LWQPTFLQAPARRPVPGDPRGKAQEAWALLVCPRR"
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/tissue_type="testls"
/clone_lib="4.34 (synonym: htes3). Vector pSport1; host
DH10B; sites_NotI + SalI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="hypothetical protein"
/protein_id="CAB70710.1"
/db_xref="GI:6807877"
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/note="DKFZp586J0619, partial"
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                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 14896) Sulston, J.E. and Waterston, R. Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
              Waterston, R.H.
                                       Du,H. and Kozlowicz,A.
The sequence of Homo sapiens BAC clone RP11-1246C19
Unpublished (2001)
Direct Submission
                                                                                                 9847074
                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                 Homo sapiens BAC clone RP11-1246C19 from 7, complete sequence.
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                       (bases 1 to 148996)
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                                                                                                                    Submitted (01-JUN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Jun 1, 2002 this sequence version replaced gi:19774660.
                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (28-MAR-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                              Submitted (30-MAR-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (22-FEB-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                          Waterston, R.
                                                                                                                                                                                                                                                                               University,
                                                                                                                                                                                                                                                                                                                     Direct Submission
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                                                                                                                                                                                                                                                                                                                                             Waterston, R.
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                                                                                                                                                                                                                                                             (bases
Center project name: H_NH1246C19
                     Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
------ Summary Statistics
                                                                                                  Center: Washington University Genome Sequencing Center
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                                                                                          Center code: WUGSC
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                                                                                                                                                                                                                                                                                                                                                          to 148996)
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions

all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by This sequence was finished as follows unless otherwise noted:

MAPPING INFORMATION:

The sequence of this clone was established as part of a mapping and sequencing collaboration between the MHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DHR/GTB/CHR7, send mailto:egreen@nhgr1.nih.gov , or see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E. Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and Coworkers at http://www.chori.org

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-369D24, 2000 by overlap, the clone sequenced to the right is RP11-16P10, 2000 by overlap, actual start of this clone is at base position 174583 of RP11-369D24; actual end is at base position 63205 of RP11-16P10.

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Sequence derived from one plasmid subclone, base position 32899 to 33087.
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FEATURES repeat_region source Unresolved tandem repeat from base position 99549 to 100076. /rpt_family="MIR" 16148. .16439 /rpt_family="Alu" 15194. .15288 /rpt_family="Alu" 14794. .14822 /clone="RP11-1246C19" /clone_lib="RPCI-11" 585. .893 rpt_family="L2" 11484. .11545 rpt_family="MER1_type" 0227. .10366 /rpt_family="Alu"
9418. .9677 rpt_family="(TTCC)n" 927. . 10207 938. .7061 'rpt_family="L1" rpt_family="MER1_type" 256...7559 /Organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="7" /map="7" rpt_family="MIR" 347. .3438 rpt_family="Alu" rpt_family="Alu" rpt_family="MIR" 708. .2769 rpt_family="Alu" t_family="Alu"
32. .14451
t_family="MIR" c_family="L1" 9. .6933 t_family="L2" 3. .9876 _family="MIR" _family="AT_rich" 8. .15133 _family="MER1_type" _family="Alu" _family="Alu" _family="L1" _family="Alu" family="MIR" [. .12259 _family="Alu" _family="Alu" . .5037 _family="L1" _family="MIR"

ACCESSION VERSION

AC120290 144097 bp DNA linear HTG 23-JUL-2002 **** 72 unordered pieces.
AC120290 AC120290 GI:21902868

KEYWORDS SOURCE

HTG; HTGS_PHASE1.
Rattus norvegicus.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bouck, J., Bowie, S., Brieva, M., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Bluhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carren, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowhiry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., P., Frantz, P., Frantz, P., Frantz, P., Frantz, P., Frantz, P., Hame, J., Jackson, L. E., Jacobson, B., Jia, Y., Johnson, R., Dolivet, S., Joudah, S., Kartovic, R., Kurshi, A., Landry, N., Leal, B., Lewis, L.C., Levis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, G., Merzker, M., Mansey, E., Martin, R., Martindale, A., Martinez, E., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Mayuen, M., Morris, S., Mayuen, A., Martin, R., Martindale, A., Martinez, E., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Mayuen, M., Morsey, M., Pulla, R., Martindale, A., Martinez, E., Mohabbat, K., Morgan, M., Morris, S., Mayuen, M., Morsey, M., Policer, M., Parez, J., Perez, J., Paters, M., Paters, M., Paters, M., Ren, Y., Scherer, S., Sottt, G., Shen, H., Shooshtari, N., Stanley, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone,
                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (23-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 18, 2002 this sequence version replaced gi:20452937.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (05-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 144097)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 144097)
                                                                                                                                                                                            Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
                                                                                                                           Center project name: GWWB
Center clone name: CH230-101110
Chemistry: Dye-terminator Big Dye: 100% of reads
                                                     Sequencing vector: Plasmid;
                                                                                                                                                                                                                                                                                                                        Center code: BCM
                                                                                                                                                                                                                                                                                                                                               Center: Baylor College of Medicine
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                                                                                                                                                                                                                                                                                                                                                                                     ----- Genome Center
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Assembly program: Phrap; version 0.990329
Consensus quality: 62007 bases at least Q40
Consensus quality: 68326 bases at least Q30
Consensus quality: 68326 bases at least Q30

**NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

**NOTE: This is a "working draft' sequence. It currently
**consists of 72 contigs. The true order of the pieces
**is not known and their order in this sequence record is
** arbitrary Gaps between the contigs are represented as
** runs of N, but the exact sizes of the gaps are unknown.
** This record will be updated with the finished sequence
** as soon as it is available and the accession number will
** be preserved.

1 1061 contig of 1060 bp in length
1161 2270: contig of Illo bp in length
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34545 35825 35925 37319 37419 38685 38785 30073 31568 31668 33102 33202 28679 29973 25498 27046 24255 24355 25398 20567 20667 5993 6093 7671 7771 9213 9313 10542 10642 12073 12173 22088 13653 15097 15197 15197 16223 16323 17656 17756 18940 19040 1061 1161 2271 4835 0: contig of 1060 bp in length
0: spa of unknown length
0: contig of 1110 bp in length
0: spa of unknown length
1: contig of 1001 bp in length
1: spa of unknown length
1: spa of unknown length
4: contig of 1363 bp in length
4: spa of unknown length
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5: contig of 1058 bp in length gap of contig gap of gap of contig gap of gap of contig gap of conti gap of contig gap or gap of gap of gap of contig gap of gap of gap of contig gap of contig gap of contig gap of contig contig contig gap o: contig gap or gap of gap of gap of contig contic contig contig gap o gap of contig of 1635 unknown unknown of 1266 unknown of 1243 unknown of 1434 unknown of 1548 unknown of 1043 f unknown g of 1321 f unknown g of 1527 f unknown g of 1333 f unknown g of 1184 f unknown g of 1229 f unknown g of 1431 unknown of 1444 unknown of 1380 f unknown g of 1442 of 1394 unknown of 1495 of 1294 unknown of 1433 of 1035 of 1032 unknown unknown unknown of 1026 unknown of 1578 unknown ni đợ bp in length bp in length ģ bp in bp in 1 length bp in] bp in l bp in] Length length ďď Length ni đq bp in length length length Length bp in pp in ength .ength Length in length in length Length

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Query Match
Best Local Sim
Matches 219;
                                                                                                                                                                                                                                                                          51563 TCCAGATCTTCCCACTGAGCCCGGATCCACGGTGGCAGAGCTCCAGTCCGCGCCCCTTG 51504
                              51323
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                                                                                                                                                                                                           51503 CCCTGGCACTGCAGCAAGCCCTGGGCCAAGAGTTGGCTCGTGTCCGGCCAGGGCAACCCCG 51444
                                                                                              51383
                                        872 GCCAGCTCTGCCAGTACCAG 891
                                                                                                                             812
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                                                                                                                                                                                                                             692 CCCTCGCCCTGCAGCACGCCCTGGGCCAGGAGCTGGCCCGCGTCGTCCAGGGCAGCCCCC 751
                                                                                                                                                                                                                                                                                                         632 TCCAGATTITCCCGCTCAGCCCGGACCCTCGGTGGCAGAGCTCCAGTCCCCGCCCCGTGG 691
                                                                                                              ACGGCGGTGCCCTGGTGATGTCCATGCACCGTAGCCACTTCCTGGCCTGCCCGCTGCTGC 871
                       GCCAGCTCTGCCAGTACCAG 51304
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9: contig of 1305 bp in length
9: gap of unknown length
0: contig of 3141 bp in length
0: gap of unknown length
6: gap of unknown length
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contig of 1861;
gap of unknown;
contig of 1328;
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                                                                                                                                                                                                                                                                                                                                                           Score 194.4; DB 2
Pred. No. 9.3e-19;
                                                                                                                                                                                                                                                                                                                                              Mismatches
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of 2081
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g of 2058
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g of 1717
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing vector: plasmid; 100% chemistry: Dye-primer ET; 0% of reads chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 consensus quality: 217436 bases at least Q40 Consensus quality: 217966 bases at least Q30 consensus quality: 218400 bases at least Q30
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(bases I to 219964)
(chases I to 219964)
McPherson,J.D. and Waterston,R.H.
Direct Submission
Submitted (08-AUG-2002) Genome Sequencing Center, 4444 Forest Park
Submitted (08-AUG-2003) Genome Sequencing Center, 4444 Forest Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center project name: M_BA0168E11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing vector: M13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC130221 219964 bp DNA linear HTG 08-A:
Mus musculus chromosome UNK clone RP23-168E11, WORKING DRAFT
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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MCPherson, J.D. and Waterston, R.H.
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/note="assembly_name:Contig14"
/note="assembly_name:Contig15"
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                                                               /note="assembly_name:Contig13"
                                                                                                                                 /organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                                      /clone="RP23-168E11"
                                                                                                                       'chromosome="UNK"
                                                                                                                                                                                       ocation,
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219964: contig of 91541 bp i
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                                                                                                 Unpublished (1997)

2 (bases I to 148432)

Celniker, S. B., Aghavani, A., Arcaina, T. T., Baxter, E., Blazej, R.G., Chew, M., Doyle, C.M., Farfan, D.E., Flanagan, J., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, S. H., Lee, B., Lomotan, M.A., Mazda, P., Mok, M.S., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfoiffer, B., Punch, D., Snir, E., Twomey, B., Wan, K.H., Whitelaw, K.R., Yee, A., Zhang, R., Zieran, L.L.
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Submitted (01-MAY-1998) Berkeley Drosophila Genome Project, MS 64-121, Lawrence Berkeley National Laboratory, One Cyclotron Road,
                                                                                                                                                                                                                                                                                                                                                               Celniker, S. E., Aghavani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Chew, M., Doyle, C.M., Farfan, D.E., Flanagan, J., Houston, K.A., Elummasti, S.R., Karra, K., Kearney, L., Kim, S.H., Lee, B., Lomotan, M.A., Mazda, P., Mok, M.S., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Punch, D., Snir, E., Twomey, B., Wan, K.H., Whitelaw, K.R., Yee, A., Zhang, R., Zieran, L.L.
                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                         Sequencing of Drosophila chromosome 2R, region 60B1-60B10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D$02867 (D200)), complete sequence.

AC004642 AC000352 AC003551 AC003553 AC003554 AC003555

AC003556 AC003557 AC003558 AC003584 AC003848 AC003849

AC003576 AC003577 AC003578 AC003579 AC003580 AC003581 AC003584

AC003583 AC003584 AC003585 AC003590 AC003586 AC003587

AC003588 AC003590 AC003591 AC003592
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster
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148432 bp DNA linear INV 01-M Drosophila melanogaster DNA sequence (PIs DS00543 (D193) and D$02867 (D200)), comblete sequence.
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80149. .128323
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                                                             Celniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H., Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C., Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A., Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M., Champe, M., Davenport, L.B., Dietz, S.M.,
Dodson,K., Dorsett,V., Doup,L.E., Doyle,C., Dresnek,D., Farfan,D., Ferriera,S., Frise,E., Galle,R.F., Garg,N.S., George,R.A., Gonzalez,M., Houck,J., Hoskins,R.A., Hostin,D., Howland,T.J.,
                                                                                                                                                                                                                                                                                                                                                                                            AC099018 154840 pp L
Drosophila melanogaster, chromosome
                                                                                                                                                                            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Meopter; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophildae; Drosophila.

[ bases 1 to 154840)
                                                                                                                                                                                                                                                                 Drosophila melanogaster
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Library locations: 63_6, 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            For further information about this sequence, including its location and relationship to other sequences, please visit our sequence
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/note="d193 extends from bp 1 to bp 83271 and d200 extends
from bp 81802 to bp 148432."
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/db_xref="taxon:7227"
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Db 133168 TACTGGAGCAGTTTGATCTGGTGAAGAATGCCATTCTGAACAAGGCCTATCTGGCCCAGC 133227
                                                                                                                                Db 133108 AAAACTTTGGCACGCCGGTCAACTCGATGTCCAAGCTGCTGGCAATGCTGGACACCGCTG 133167
                                                                                                                                                                                                                                                                    Db 133048 ACAGACTAATTGAGGCAGCTCTCAACGATCTAACGCCGGATCAGATCGTGCTCTTTGTGC 133107
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Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C.,
Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A.,
Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M.,
Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D.,
Ferriera, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A.,
Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J.,
Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattel, B., Moshrefi, A.,
McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Numoo, J.,
Pacleb, J., Paragas, V., Park, S., Patel, S., Pfeiffer, B.,
Phouanenavong, S., Pittman, G.S., Puti, V., Richards, S., Scheeler, F.,
Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M.,
Direct Submission
Direct Submission.
                                       TGGCCCACGCCCCAGACTCTGGAGCAGAACATCATGGACAAGAATTACATGGCCCACC 427
                                                                                                                                                                                                    AGTCGTTTGGCATCCCCGTGTCCAGCATGAGCAAACTCCTCCAGTTCCTGGACCAGGCAG 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattei, B., Moshrefi, A., McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Patel, S., Pfeiffer, B., Phouanenavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F., Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M., Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C. Sequencing of Drosophila chromosome 2R, region 60A-60B
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/clone=lib="TRCI-98 (Roswell Park Cancer Institute
Drosophila melanogaster BAC library, partial EcoRI in
pBACe3.6)"
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/strain="y; cn bw sp"
/db_xref="taxon:7227"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 133228 TAATCGAGATTCAGCAGGCGCGGGGTGC 133255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC020509/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                              81998 TAATCGAGATTCAGCAGGCGCGGGGTGC 81971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAI
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                                                                                                                                                                                                                                                     82058 TACTGGAGCAGTTTGATCTGGTGAAGAATGCCATTCTGAACAAGGCCTATCTGGCCCCAGC 81999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                      82178 ACAGACTAATTGAGGCAGCTCTCAACGATCTAACGCCGGATCAGATCGTGCTCTTTGTGC 82119
                                                                                                                                                                                                                                                                                                                                      82118 AAAACTTTGGCACGCCGGTCAACTCGATGTCCAAGCTGCTGGCAATGCTGGACACCGCTG 82059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82238 AGGAGCÀGGTGCAACTGCTGCCCGACTGGCTGAAGCTGAAGATGATCCGCTCATCGGTGG 82179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82298 TGGACTATTGGTTTCCGCCCGGACGACCAGCGCCCGTCGCCTTTCTGCCCCAGCATGCCGC 82239
                                                                                                                                                                                                                    428 TGGTGGAGGTCCAGCATGAGCGCGGCGC 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             188 CGGAGGAGCTGCTGCTTCCTGACTGGCTGAAGCTGCGCATGATCCGTTCTGAGGTGC 247
                                                                                                                                                                                                                                                                                                                                                                             308 AGTCGTTTGGCATCCCCGTGTCCAGCATGAGCAAACTCCTCCAGTTCCTGGACCAGGCAG 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                               248 TOCGCCTGGTGGACGCCGCCCTGCAGGACCTGGAGCCGCAGCAGCTGCTGCTGTTCGTGC 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131 TGGACATCTGGTTTCCGGAGGAGAAGCCACTGCCCACCGCCTTCCTGGTGGACA----CAT 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
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                                                                                                                                                                                                                                                                                           TGGCCCACGACCCCCAGACTCTGGAGCAGAACATCATGGACAAGAATTACATGGCCCACC 427
  complete sequence.
AE003462 AE013599 AE002575
AE003462.2 GI:21626662
                                                   Drosophila melanogaster 2R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence was identified as CDM:10213488 by the submitter. For more information on this record e-mail to fly@celera.com. * NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission Submitted (30-DEC-1999) Celera Genomics, 45 West Gude Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster. Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rockville, MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Meopter; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroides; Drosophilidae; Drosophila.

1 (bases 1 to 157851)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACO20509 157851 bp DNA linear HTG 03-UAN-2000 Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adams, M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HTG; HTGS_PHASE2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC020509.1 GI:6664388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
41166 a 36910 c 37402 g 42373 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                by the finished sequence as soon as it is available and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
GI:21626662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.1%; Score 107.2; DB 2; 60.1%; Pred. No. 2.4e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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                                                                           303823 bp
                                                       section
                                        DNA linear INV 28-JUN-20
70 of 74 of the complete arm,
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Hernandez, J.R., Houck, J., Hostin, D., Houston, K.A., Howland, T.J.,
Wei, M.H., Ibegwam, C., Jalali, M., Kalush, F., Karpen, G.H., Ke, Z.,
Kennison, J.A., Ketchum, K.A., Kimmel, B.E., Kodira, C.D., Kraft, C.,
Krawitz, S., Kulp, D., Lai, Z., Lasko, P., Lei, Y., Levitsky, A.A.,
Li, J., Li, Z., Liang, Y., Lin, X., Liu, X., Mattei, B., WcIntosh, T.C.,
McIcod, M.P., Mogherson, D., Merkulov, G., Milshina, N.V., Mobarry, C.,
Muzny, D.M., Nelson, D.L., Nelson, D.R., Mishina, N.V., Mobarry, C.,
Muzny, D.M., Nelson, D.L., Nelson, D.R., Pittman, G.S., Pan, S.,
Sunders, R.D., Scheeler, F., Shen, H., Shue, B.C., Siden-Kiamos, I.,
Simpson, M., Skupski, M.P., Smith, T., Spier, E., Spradling, A.C.,
Yenter, E., Wang, A.H., Wang, X., Wang, Z.Y., Wassarman, D.A.,
Weinstock, G.M., Weissenbach, J., Williams, S.M., Woodage, T.,
Zaveri, J.S., Lhan, M., Zhang, G., Zhao, Q., Zheng, L., Zheng, X.H.,
Gibbs, R.A., Myers, E.W., Rubin, G.M. and Venter, J.C.

The genome sequence of Drosophila melanogaster

NEE 2019606
                                                                                 Misra, S., Crosby, M.A., Matthews, B.B., Bayraktaroglu, L., Campbell, K., Hradecky, P., Huang, Y., Kaminker, J.S., Prochnik, S.E., Smith, C.D., Tupy, J.L., Bergman, C.M., Berman, B.P., Carlson, J.W., Calniker, S.E., Clamp, M.E., Drysdale, R.A., Emmert, D., Frise, E., de Grey, A.D.N.J., Harris, N.L., Krommiller, B., Marshall, B., Milburn, G.H., Richter, J., Russo, S., Searle, S.M.J., Smith, E., Shu, S., Smuthiak, F., Whitfield, E.J., Yamada, C., Ashburner, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Doup, I.E., Doyle, C., Dresnek, D., Farfan, D., Ferriera, S., Frise, E., dalle, R.F., Garg, N.S., George, R.A., Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J., Ibegvan, C., Jalali, M., Kruse, D., Li, P., Mattel, B., Moshrefi, A., McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunco, J., Pacleb, J., Paragas, V., Park, S., Fatel, S., Feiffer, B., Phouanenavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F., Stapleton, M., Strong, R., Smith, H.O., Venter, J.C., and Rubin, G.M., Zaveri, J.S., Smith, H.O., Venter, J.C., and Rubin, G.M.
                                              Gelbart, W.M., Rubin, G.M., Mungall, C.J. and Lewis, S.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing of Drosophila melanogaster genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Benos, P.V., Berman, B.P., Bhandari, D., Bolshakov, S., Borkova, D., Botthan, M.R., Bouck, J., Brokstein, P., Brottier, P., Burtis, K.C., Busam, D.A., Butler, H., Cadieu, E., Center, A., Chandra, I., Cherry, J.M., Cawley, S., Dahlke, C., Davenport, L.B., Davies, P., de Pablos, B., Delcher, A., Deng, Z., Mays, A.D., Dew, L., Dietz, S.M., Dodson, K., Doup, L.E., Downes, M., Dugan-Rocha, S., Dunkov, B.C., Dunn, P., Durbin, K.J., Evangelista, C.C., Ferraz, C., Ferriera, S., Villette, A., Control of the property of the proper
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Gelbart, W.M., Glasser, K., Glodek, A., Gong, F., Gorrell, J.H., Gu, Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sutton, G.G., Wortman, J.R., Yandell, M.D., Zhang, Q., Chen, L.X., Brandon, R.C., Rogers, Y.H., Blazej, R.G., Champe, M., Pfeiffer, B.D., Wan, K.H., Doyle, C., Baxter, E.G., Helt, G., Nelson, C.R., Gabor Miklos, G.I., Abril, J.F., Agbayani, A., An, H.J., Andrews-Pfannkoch, C., Baldwin, D., Ballew, R.M., Basu, A., Bayraktarogin, L., Beasey, E.M., Beeson, K.Y., Benne, D. V., Renne, D. V., Renn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 (bases 1 to 303823)
Adams, M.D., Celniker, S.E., Gibbs, R.A., Rubin, G.M. and Venter, C.J.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rockville, MD,
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                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="flybase:fban0015800"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="FIYBASE:FBan0011169"
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                                                                  product="CG30177-RA"
                                                                                                                                                                                                                                                                                                                        map="60A10-60A10"
                                                                                                                                                                                                                                                                                                                                                                      /gene="CG30177"
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/db_xref="G1:7291639"
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/product="CG15800-RA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="FLYBASE:FBgn0034904"
complement(16742. .17216)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(16742. .17216)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(join(11873. .12379,18020. .18091))
/gene="CG11169"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                db_xref="FLYBASE:FBan0015800"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="FLYBASE:FBgn0034905"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="CG11169-RA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="CG11169"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /chromosome="2"
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Db 267802 TACTGGAGCAGTTTGATCTGGTGAAGAATGCCAFTCTGAACAAGGCCTATCTGGCCCAGC 267861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 267622 AGGAGCAGGTGCAACTGCTGCCCGACTGGCTGAAGCTGAAGATGATCCGCTCATCGGTGG 267681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 267562 TGGACTATTGGTTTCCGCCCGGACGACCAGCCCGTCGCCTTTCTGCCCAGCATGCCGC 267621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Simi
Matches 197;
                                                                                                                                                            267742 AAAACTTTGGCACGCCGGTCAACTCGATGTCCAAGCTGCTGGCAATGCTGGACACCGCTG 267801
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                                                                                                                                                                                                                308 AGTCGTTTGGCATCCCCGTGTCCAGCATGAGCAAACTCCTCCAGTTCCTGGACCAGGCAG 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  188 CGGAGGAGGCGCTGCTTCCTGACTGGCTGAAGCTGCGCATGATCCGTTCTGAGGTGC 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131 TGGACATCTGGTTTCCGGAGGAGAAGCCACTGCCCACCGCCTTCCTGGTGGACA---CAT 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA
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                                               TGGCCCACGACCCCCAGACTCTGGAGCAGAAGATCATGGACAAGAATTACATGGCCCACC 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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ilarity 60.1%;
Conservative
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31014. .31853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="CG5539"
/note="CG5539 gene product"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="FLYBASE:FBan0013561"
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27671. .28291
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/codon_start=1
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Pred. No. 2.1e-06;
0; Mismatches 128; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .30720))
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Search completed: March 24, 2003, 16:24:37 Job time: 10061 secs